



THE UNIVERSITY OF
CHICAGO

DEPARTMENT OF STATISTICS

MASTER'S THESIS PRESENTATION

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Quantifying Gene Expression Dispersion Patterns in Differentiated Human Induced Pluripotent Stem Cells

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ABSTRACT

Biological robustness relates to the ability of biological systems to maintain stable phenotypes. Currently, it is unknown how the underlying mechanisms of robustness are genetically encoded. We develop an approach that characterizes robustness as dispersion of gene expression. Specifically, the described method identifies genes that exhibit significant dispersion. We demonstrate the utility of this tool on single cell RNA-seq (scRNA-seq) data in differentiated human induced pluripotent stem cells (iPSCs) and discuss how the method can be applied across different contexts such as cell types to acquire gene sets of interest. The framework from this analysis will guide future studies that enhance our understanding of genetic control of robustness.